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## RAW SEQUENCE LISTING

DATE: 07/23/2002

PATENT APPLICATION: US/10/058,053A

TIME: 15:59:19

Input Set : A:\2314-248-rev.ST25.txt

Output Set: N:\CRF3\07232002\J058053A.raw

3 <110> APPLICANT: University of Utah Research Foundation  
 4 Cognetix, Inc.  
 5 Jones, Robert M.  
 6 Garrett, James E.  
 7 Watkins, Maren  
 8 Olivera, Baldomero M.  
 10 <120> TITLE OF INVENTION: B-Superfamily Conotoxins  
 12 <130> FILE REFERENCE: 2314-248  
 14 <140> CURRENT APPLICATION NUMBER: US 10/058,053A  
 C--> 15 <141> CURRENT FILING DATE: 2002-07-05  
 17 <150> PRIOR APPLICATION NUMBER: US 60/264323  
 18 <151> PRIOR FILING DATE: 2001-01-29  
 20 <160> NUMBER OF SEQ ID NOS: 340  
 22 <170> SOFTWARE: PatentIn version 3.0  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 456  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Conus flavidus  
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 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (7)..(255)  
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 35 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Val Trp  
 36 1 5 10  
 38 att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att cgg 96  
 39 Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg  
 40 15 20 25 30  
 42 ggt ttg gtg cca gat gac tta acc cca cag ctt att ttg caa agt ctg 144  
 43 Gly Leu Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Gln Ser Leu  
 44 35 40 45  
 46 gat tcc cgt cgt cat gat cac ggc att cgt ccg aag aga gtc gac ata 192  
 47 Asp Ser Arg Arg His Asp His Gly Ile Arg Pro Lys Arg Val Asp Ile  
 48 50 55 60  
 50 tgt aac tgg agg ata tgt gca cca aac cca ttg aga cga cat gat ctt 240  
 51 Cys Asn Trp Arg Ile Cys Ala Pro Asn Pro Leu Arg Arg His Asp Leu  
 52 65 70 75  
 54 aag aaa gga aac aat tgacgtcaga caaccgccac aacttgagta cgacatcgtt 295  
 55 Lys Lys Gly Asn Asn  
 56 80  
 58 aatacgactt cagcaaatat gaaattttca gcatcactgt ggttgtgaag aaatcagttg 355  
 60 ctttaaaagg ttggatttgt ccttggttaa gccgttgtac tgatgacatc tctgcactat 415  
 62 gaaataaagc tgatgtgaca aactaaaaaa aaaaaaaaaa a 456

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Input Set : A:\2314-248-rev.ST25.txt

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65 <210> SEQ ID NO: 2
66 <211> LENGTH: 83
67 <212> TYPE: PRT
68 <213> ORGANISM: Conus flavidus
70 <400> SEQUENCE: 2
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73 1 5 10 15
76 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
77 20 25 30
80 Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Gln Ser Leu Asp Ser
81 35 40 45
84 Arg Arg His Asp His Gly Ile Arg Pro Lys Arg Val Asp Ile Cys Asn
85 50 55 60
88 Trp Arg Ile Cys Ala Pro Asn Pro Leu Arg Arg His Asp Leu Lys Lys
89 65 70 75 80
92 Gly Asn Asn
96 <210> SEQ ID NO: 3
97 <211> LENGTH: 33
98 <212> TYPE: PRT
99 <213> ORGANISM: Conus flavidus
101 <220> FEATURE:
102 <221> NAME/KEY: PEPTIDE
103 <222> LOCATION: (1)..(33)
104 <223> OTHER INFORMATION: Xaa at residues 7, 20 and 22 may be Pro or hydroxy-Pro; Xaa
at re
105 sideue 15 may be Trp (Dor L) or bromo-Trp (Dor L)
108 <400> SEQUENCE: 3
W-1> 110 His Asp His Gly Ile Arg Xaa Lys Arg Val Asp Ile Cys Asn Xaa Arg
W-1> 111 1 5 10 15
W-1> 113 Ile Cys Ala Xaa Asn Xaa Leu Arg Arg His Asp Leu Lys Lys Gly Asn
114 20 25 30
116 Asn
119 <210> SEQ ID NO: 4
120 <211> LENGTH: 374
121 <212> TYPE: DNA
122 <213> ORGANISM: Conus miles
124 <220> FEATURE:
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126 <222> LOCATION: (7)..(315)
128 <400> SEQUENCE: 4
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131 1 5 10
133 ggg ctc acc gtc ggg agt cac gtc cat cgg tct cac agt cct aca tcg 96
134 Gly Leu Thr Val Gly Ser His Val His Arg Ser His Ser Pro Thr Ser
135 15 20 25 30
137 cgc agc cat ggt gat gac tcc att cat gac aag acg att cat caa cat 144
138 Arg Ser His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His
139 35 40 45
141 ctg ttt gcc cgt ctt cct ctg gag aac aac gac gac cat cgt tct gtg 192

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142 Leu Phe Ala Arg Leu Pro Leu Glu Asn Asn Asp Asp His Arg Ser Val
143          50          55          60
145 gat ctt cct gca ggg aat ggt gca ggc aac acc aag caa caa gac caa      240
146 Asp Leu Pro Ala Gly Asn Gly Ala Gly Asn Thr Lys Gln Gln Asp Gln
147          65          70          75
149 agt cct cat cat gtg tgt tgt gct att ggt ccg gtt ctt cca ttc tgt      288
150 Ser Pro His His Val Cys Cys Ala Ile Gly Pro Val Leu Pro Phe Cys
151          80          85          90
153 tgt gtc agt tgg ctg cac aaa ctc cat tgaactggcc aatgaaaata      335
154 Cys Val Ser Trp Leu His Lys Leu His
155 95          100
157 actcaggaat agacagaaaag gcaaaaaaaaa aaaaaaaaaa      374
160 <210> SEQ ID NO: 5
161 <211> LENGTH: 103
162 <212> TYPE: PRT
163 <213> ORGANISM: Conus miles
165 <400> SEQUENCE: 5
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168 1          5          10          15
171 Thr Val Gly Ser His Val His Arg Ser His Ser Pro Thr Ser Arg Ser
172          20          25          30
175 His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His Leu Phe
176          35          40          45
179 Ala Arg Leu Pro Leu Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu
180          50          55          60
183 Pro Ala Gly Asn Gly Ala Gly Asn Thr Lys Gln Gln Asp Gln Ser Pro
184 65          70          75          80
187 His His Val Cys Cys Ala Ile Gly Pro Val Leu Pro Phe Cys Cys Val
188          85          90          95
191 Ser Trp Leu His Lys Leu His
192          100
195 <210> SEQ ID NO: 6
196 <211> LENGTH: 29
197 <212> TYPE: PRT
198 <213> ORGANISM: Conus miles
200 <220> FEATURE:
201 <221> NAME/KEY: PEPTIDE
202 <222> LOCATION: (1)..(29)
203 <223> OTHER INFORMATION: Xaa at residue 1 is Gln or pyro-Glu; Xaa at residues 6, 15
and 18
204          may be Pro or hydroxy-Pro; Xaa at residue 24 may be Trp (D or L)
205          or bromo-Trp (D or L)
208 <400> SEQUENCE: 6
W--> 210 Xaa Gln Asp Gln Ser Xaa His His Val Cys Cys Ala Ile Gly Xaa Val
211 1          5          10          15
W--> 213 Leu Xaa Phe Cys Cys Val Ser Xaa Leu His Lys Leu His
214          20          25
216 <210> SEQ ID NO: 7
217 <211> LENGTH: 359
218 <212> TYPE: DNA

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Output Set: N:\CRF3\07232002\J058053A.raw

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219 <213> ORGANISM: Conus miles
221 <220> FEATURE:
222 <221> NAME/KEY: CDS
223 <222> LOCATION: (7)..(291)
225 <400> SEQUENCE: 7
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227      Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val
228      1          5          10
230 ggg ttc acc gtc ggg ggt cac gtc cat cgg tct cac agt cct aca tcg      96
231 Gly Phe Thr Val Gly Gly His Val His Arg Ser His Ser Pro Thr Ser
232 15          20          25          30
234 cgc agc agc cat ggt gat gac tcc att cat gac aag acg att cat caa cat      144
235 Arg Ser His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His
236          35          40          45
238 ctg ttt gcc cgt ctt cct cag gag aac aac gac gac cat cgt tct gtg      192
239 Leu Phe Ala Arg Leu Pro Gln Glu Asn Asn Asp Asp His Arg Ser Val
240          50          55          60
242 gat ctt cct gca ggg act agc gca ggc gac atg aaa cca caa cgc caa      240
243 Asp Leu Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln
244          65          70          75
246 aga cgt ctg tgc tgc atc ttt gcc ccg att ctt tgg ttc tgt tgt cac      288
247 Arg Arg Leu Cys Cys Ile Phe Ala Pro Ile Leu Trp Phe Cys Cys His
248          80          85          90
250 ggt taacagctca aattacactg cactggccga ttgaaagaac tgcaataaac      341
251 Gly
252 95
254 ggaaaaaaaaa aaaaaaaaaa      359
257 <210> SEQ ID NO: 8
258 <211> LENGTH: 95
259 <212> TYPE: PRT
260 <213> ORGANISM: Conus miles
262 <400> SEQUENCE: 8
264 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Gly Phe
265 1          5          10          15
268 Thr Val Gly Gly His Val His Arg Ser His Ser Pro Thr Ser Arg Ser
269          20          25          30
272 His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His Leu Phe
273          35          40          45
276 Ala Arg Leu Pro Gln Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu
277          50          55          60
280 Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln Arg Arg
281 65          70          75          80
284 Leu Cys Cys Ile Phe Ala Pro Ile Leu Trp Phe Cys Cys His Gly
285          85          90          95
288 <210> SEQ ID NO: 9
289 <211> LENGTH: 14
290 <212> TYPE: PRT
291 <213> ORGANISM: Conus miles
293 <220> FEATURE:

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## RAW SEQUENCE LISTING

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TIME: 15:59:19

Input Set : A:\2314-248-rev.ST25.txt

Output Set: N:\CRF3\07232002\J058053A.raw

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294 <221> NAME/KEY: PEPTIDE
295 <222> LOCATION: (1)..(14)
296 <223> OTHER INFORMATION: Xaa at residue 7 may be Pro or hydroxy-Pro; Xaa at residue
10 may
297      be Trp (D or L) or bromo-Trp (D or L)
300 <400> SEQUENCE: 9
302 Leu Cys Cys Ile Phe Ala Xaa Ile Leu Xaa Phe Cys Cys His
303 1          5          10
305 <210> SEQ ID NO: 10
306 <211> LENGTH: 351
307 <212> TYPE: DNA
308 <213> ORGANISM: Conus capitaneus
310 <220> FEATURE:
311 <221> NAME/KEY: CDS
312 <222> LOCATION: (7)..(291)
314 <400> SEQUENCE: 10
315 ggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg gtg      48
316      Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val
317      1          5          10
319 ggg ttc acc gtc ggg ggt cac gtc cat cgg tct cac agt cct aca tcg      96
320 Gly Phe Thr Val Gly Gly His Val His Arg Ser His Ser Pro Thr Ser
321 15          20          25          30
323 cgc agc cat ggt gat gac tcc att cat gac gag acg att cat caa cat      144
324 Arg Ser His Gly Asp Asp Ser Ile His Asp Glu Thr Ile His Gln His
325      35          40          45
327 ctg ttt gcc cgt ctt cct cag gag aac aac gac gac cat cgt tct gtg      192
328 Leu Phe Ala Arg Leu Pro Gln Glu Asn Asn Asp Asp His Arg Ser Val
329      50          55          60
331 gat ctt cct gca ggg act agc gca ggc gac atg aaa cca caa cgc caa      240
332 Asp Leu Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln
333      65          70          75
335 aga ggt ttc tgc tgc gac ttt ccc ccg att ttt tgg ttc tgt tgt atc      288
336 Arg Gly Phe Cys Cys Asp Phe Pro Pro Ile Phe Trp Phe Cys Cys Ile
337      80          85          90
339 ggt taacagcaca aattacactg cactggccga ttgaaagaac tgcaataaac      341
340 Gly
341 95
343 ggaaaaaaaaa      351
346 <210> SEQ ID NO: 11
347 <211> LENGTH: 95
348 <212> TYPE: PRT
349 <213> ORGANISM: Conus capitaneus
351 <400> SEQUENCE: 11
353 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Gly Phe
354 1          5          10          15
357 Thr Val Gly Gly His Val His Arg Ser His Ser Pro Thr Ser Arg Ser
358      20          25          30
361 His Gly Asp Asp Ser Ile His Asp Glu Thr Ile His Gln His Leu Phe
362      35          40          45
365 Ala Arg Leu Pro Gln Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu

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**RAW SEQUENCE LISTING ERROR SUMMARY**  
**PATENT APPLICATION: US/10/058,053A**DATE: 07/23/2002  
TIME: 15:59:20Input Set : A:\2314-248-rev.ST25.txt  
Output Set: N:\CRF3\07232002\J058053A.raw**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 7,15,20,22  
Seq#:6; Xaa Pos. 1,6,15,18,24  
Seq#:9; Xaa Pos. 7,10  
Seq#:12; Xaa Pos. 7,8,11  
Seq#:15; Xaa Pos. 7,11,16,17  
Seq#:16; N Pos. 347,385,386  
Seq#:18; Xaa Pos. 7,15,20,26,27,29  
Seq#:21; Xaa Pos. 16,20,21,23  
Seq#:24; Xaa Pos. 16,20,21,23,24,27  
Seq#:27; Xaa Pos. 10,16,20,21,23,24  
Seq#:28; N Pos. 425,426  
Seq#:30; Xaa Pos. 7,10,14,18,19,21  
Seq#:33; Xaa Pos. 1,7,14,16,17,24,28,29,31,32,33,34  
Seq#:36; Xaa Pos. 1,7,9,14,20,21,29,30,33,43  
Seq#:39; Xaa Pos. 11,13,14,19  
Seq#:42; Xaa Pos. 1,14,16,17,24,28,29,31,32,33,34  
Seq#:45; Xaa Pos. 7,15,19,20,22,23  
Seq#:48; Xaa Pos. 16,20,23,24,27  
Seq#:51; Xaa Pos. 8,10,14,18,19  
Seq#:54; Xaa Pos. 7,15,19,20,22,23  
Seq#:57; Xaa Pos. 15,25,29,30,31,32,33  
Seq#:60; Xaa Pos. 16,20,21,22,23,24  
Seq#:63; Xaa Pos. 25,29,30,32,33  
Seq#:66; Xaa Pos. 16,20,21,23,24,27  
Seq#:69; Xaa Pos. 1,3,4,5,10,14,15,16,17,18  
Seq#:72; Xaa Pos. 1,6,10,14,15,17,18  
Seq#:75; Xaa Pos. 15,19,20,22  
Seq#:78; Xaa Pos. 13,17,18,19,20  
Seq#:81; Xaa Pos. 7,11,13,14,19,37,38  
Seq#:84; Xaa Pos. 3,14,18,19,20,21,22,25  
Seq#:87; Xaa Pos. 3,14,18,19,20,21,22,25  
Seq#:90; Xaa Pos. 14,21,24,29,30,31,33,43,45  
Seq#:93; Xaa Pos. 12,17,18,20,27,30  
Seq#:96; Xaa Pos. 12,17,18,20,25,27,30  
Seq#:99; Xaa Pos. 12,17,20,27,30  
Seq#:102; Xaa Pos. 16,20,23,24,27,32  
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Seq#:108; Xaa Pos. 16,20,21,23,24  
Seq#:111; Xaa Pos. 7,10,14,18,20,21,22,24,25  
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Seq#:117; Xaa Pos. 1,7,14,16,17,24,29,31,32,33,34  
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Seq#:123; Xaa Pos. 2,14,18,19,21,25,27,29  
Seq#:126; Xaa Pos. 2,15,19,20,22,23

**RAW SEQUENCE LISTING ERROR SUMMARY**  
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Input Set : A:\2314-248-rev.ST25.txt

Output Set: N:\CRF3\07232002\J058053A.raw

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Seq#:136; N Pos. 467  
Seq#:138; Xaa Pos. 8,10,15,19,20,22  
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Seq#:142; N Pos. 582  
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Seq#:147; Xaa Pos. 1,9,12,18  
Seq#:150; Xaa Pos. 11,13,20,24,25,27,28  
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Seq#:174; Xaa Pos. 3,13,14,17,21,23,24,25,33,37  
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Seq#:189; Xaa Pos. 3,10,14,15,19,22  
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Seq#:195; Xaa Pos. 9  
Seq#:198; Xaa Pos. 14,18,19,21,22,25,27,35,36  
Seq#:201; Xaa Pos. 14,18,19,21,22  
Seq#:204; Xaa Pos. 14,18,19,21,22  
Seq#:207; Xaa Pos. 14,18,19,21,22,25  
Seq#:210; Xaa Pos. 14,18,19,21,22,25,27,35,36  
Seq#:213; Xaa Pos. 11,13,14,19  
Seq#:216; Xaa Pos. 2,15,19,20,22,23  
Seq#:219; Xaa Pos. 2,15,19,20,22,23  
Seq#:222; Xaa Pos. 7,11,16,17  
Seq#:225; Xaa Pos. 11,13,20,24,25,27,28  
Seq#:228; Xaa Pos. 7  
Seq#:308; Xaa Pos. 4

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Seq#:313; Xaa Pos. 2  
Seq#:314; Xaa Pos. 5  
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Seq#:316; Xaa Pos. 2  
Seq#:317; Xaa Pos. 5  
Seq#:318; Xaa Pos. 2,5  
Seq#:319; Xaa Pos. 4  
Seq#:320; Xaa Pos. 5  
Seq#:321; Xaa Pos. 4  
Seq#:323; Xaa Pos. 10  
Seq#:324; Xaa Pos. 5  
Seq#:325; Xaa Pos. 7  
Seq#:326; Xaa Pos. 7  
Seq#:327; Xaa Pos. 7  
Seq#:328; Xaa Pos. 13  
Seq#:329; Xaa Pos. 7  
Seq#:330; Xaa Pos. 17  
Seq#:331; Xaa Pos. 6  
Seq#:332; Xaa Pos. 6  
Seq#:333; Xaa Pos. 6  
Seq#:336; Xaa Pos. 8  
Seq#:337; Xaa Pos. 8  
Seq#:338; Xaa Pos. 2,3,5  
Seq#:339; Xaa Pos. 3